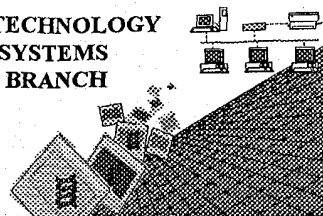


1655
BIOTECHNOLOGY
SYSTEMS
BRANCH



0590
0306

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/916,443
Source: 1600
Date Processed by STIC: 2/28/02

RECEIVED
MAR 14 2002
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

1600

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/916,443
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



1600

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/916,443

DATE: 02/28/2002
TIME: 09:00:49

Input Set : A:\2636-101.app
Output Set: N:\CRF3\02282002\I916443.raw

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

3 <110> APPLICANT: Eaton, Bruce
4 Tarasow, Theodore
6 <120> TITLE OF INVENTION: Parallel Selex
8 <130> FILE REFERENCE: 2636-108
10 <140> CURRENT APPLICATION NUMBER: 09/916,443
11 <141> CURRENT FILING DATE: 2001-07-30
13 <150> PRIOR APPLICATION NUMBER: 09/546,657
14 <151> PRIOR FILING DATE: 2000-04-10
16 <150> PRIOR APPLICATION NUMBER: 09/157,601
17 <151> PRIOR FILING DATE: 1998-09-21
19 <150> PRIOR APPLICATION NUMBER: 08/618,700
20 <151> PRIOR FILING DATE: 1996-03-20
22 <150> PRIOR APPLICATION NUMBER: 08/309,245
23 <151> PRIOR FILING DATE: 1994-09-20
25 <160> NUMBER OF SEQ ID NOS: 7
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 10
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
37 <400> SEQUENCE: 1
38 ccaggcacgc
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 87
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
49 <400> SEQUENCE: 2
50 gggagacaag aataaacgct caannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
51 nnnnttcgaca ggaggctcac aacaggc 87
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 20
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
62 <400> SEQUENCE: 3
63 cttgtctccc gcgtgcctgg 20
66 <210> SEQ ID NO: 4
67 <211> LENGTH: 77

10
Must provide location of n
and what residue n represents
- see error summary sheet,
item 9

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/916,443

DATE: 02/28/2002
 TIME: 09:00:49

Input Set : A:\2636-101.app
 Output Set: N:\CRF3\02282002\I916443.raw

```

68 <212> TYPE: RNA
69 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
74 <400> SEQUENCE: 4
W--X 75 gggagcucag aaauaacgcu caannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnuucgaca 60
76 ugaggcccg auccggc 77
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 78
81 <212> TYPE: RNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
87 <400> SEQUENCE: 5
88 gggagcucag aaauaacgcu caaagcuguu ggcagcgcug gugaagggau aggcucgac 60
89 augaggcccg gaucggc 78
92 <210> SEQ ID NO: 6
93 <211> LENGTH: 147
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
100 <400> SEQUENCE: 6
W--> 101 gggagacaag aataaacgct caannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
W--> 102 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
W--> 103 nnnnttcgaca ggaggetcac aacaggc 147
106 <210> SEQ ID NO: 7
107 <211> LENGTH: 147
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Description of Artificial Sequence:Random Sequence
114 <400> SEQUENCE: 7
W--> 115 gggagacaag aataaacgct caannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
W--> 116 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
W--> 117 nnnnttgagcg tgaggtact aacaggc 147

```

- Some
error

same

same

VERIFICATION SUMMARY . . .
PATENT APPLICATION: US/09/916,443

DATE: 02/28/2002
TIME: 09:00:50

Input Set : A:\2636-101.app
Output Set: N:\CRF3\02282002\I916443.raw

L:50 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:50 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:75 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:101 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:101 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:102 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:102 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:115 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:115 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:116 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:116 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:117 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:117 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7